

```

$ kallisto quant -i mm10 -o kallisto_output/SRR1654628 --bootstrap-samples=10 SRR1654628_1.fastq.gz
SRR1654628_2.fastq.gz -t 28

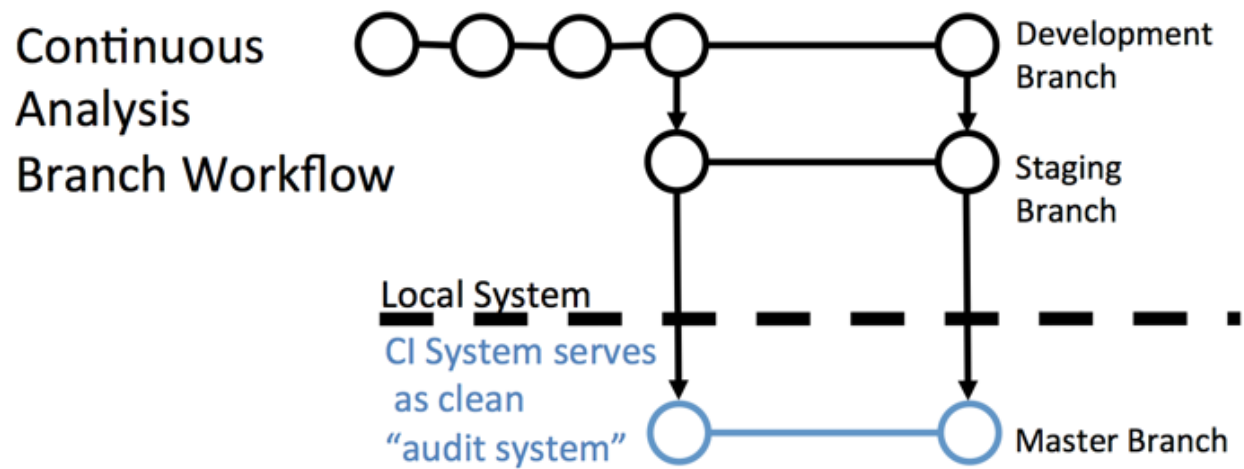
[quant] fragment length distribution will be estimated from the data
[index] k-mer length: 31
[index] number of targets: 35,026
[index] number of k-mers: 64,110,878
[index] number of equivalence classes: 81,212
[quant] running in paired-end mode
[quant] will process pair 1: SRR1654628_1.fastq.gz
                           SRR1654628_2.fastq.gz
[quant] finding pseudoalignments for the reads ... done
[quant] processed 54,088,667 reads, 35,922,079 reads pseudoaligned
[quant] estimated average fragment length: 175.781
[  em] quantifying the abundances ... done
[  em] the Expectation-Maximization algorithm ran for 1,351 rounds
[~warn] number of threads (28) greater than number of bootstraps
[~warn] (cont'd) updating threads to number of bootstraps 10
[bstrp] number of EM bootstraps complete: 1
[bstrp] number of EM bootstraps complete: 2
[bstrp] number of EM bootstraps complete: 3
[bstrp] number of EM bootstraps complete: 4
[bstrp] number of EM bootstraps complete: 5
[bstrp] number of EM bootstraps complete: 6
[bstrp] number of EM bootstraps complete: 7
[bstrp] number of EM bootstraps complete: 8
[bstrp] number of EM bootstraps complete: 9
[bstrp] number of EM bootstraps complete: 10

```

Supplementary Figure 1

Example continuous integration log.

Continuous integration log showing quantification of the abundances of RNA transcripts from RNA-seq data using Kallisto.



Supplementary Figure 2

Example continuous analysis branch workflow.

Code changes are made on development branches. When completed, changes are merged into the staging branch and continuous integration runs. If the continuous integration process succeeds, changes are merged into the master branch and pushed along with regenerated figures and results.

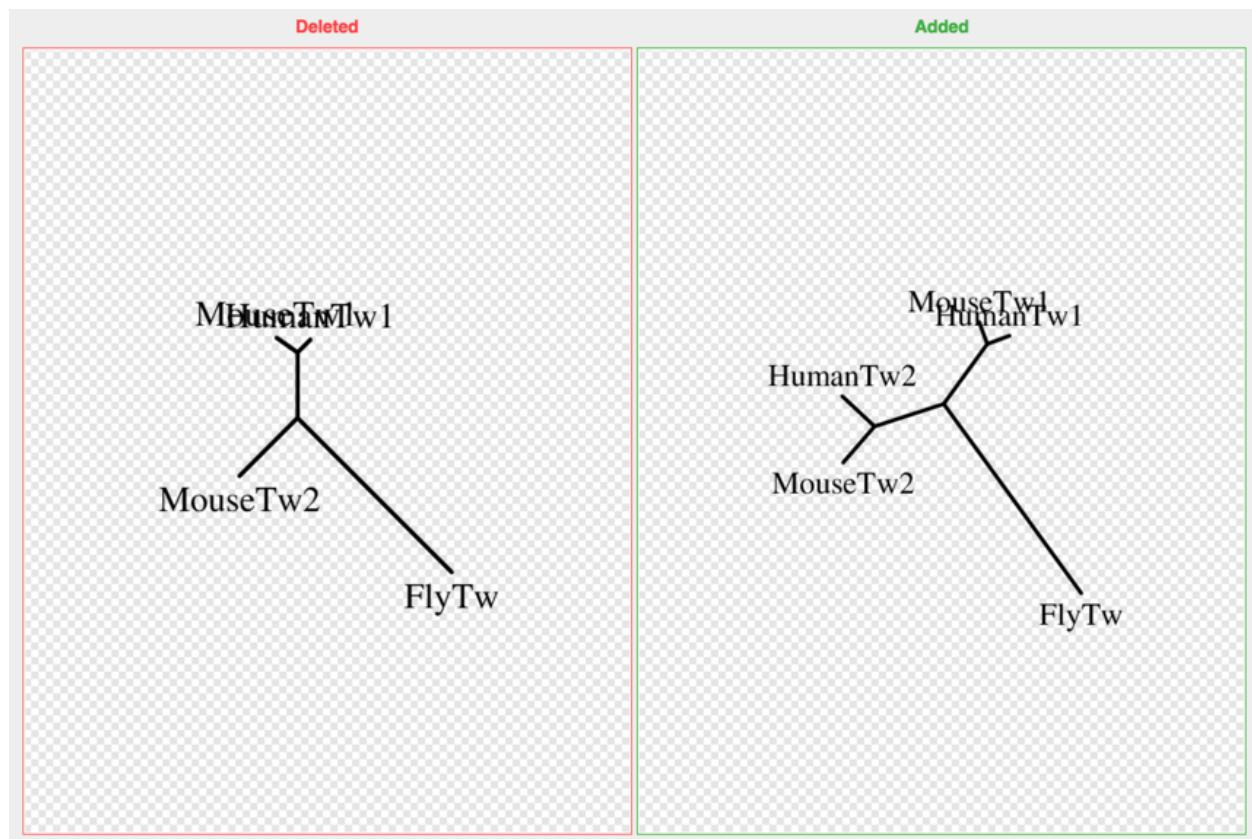
```
# choose the base docker image
image: brettbj/continuous_analysis_base
script:
  # run tests
  # perform analysis

# publish results
publish:
  docker:
    # docker details
```

Supplementary Figure 3

Example basic YAML file structure.

Example .yaml file structure, choose your Docker image, run tests, perform analysis and then publish results.



Supplementary Figure 4

Consensus phylogenetic tree tracked between two continuous analysis runs.

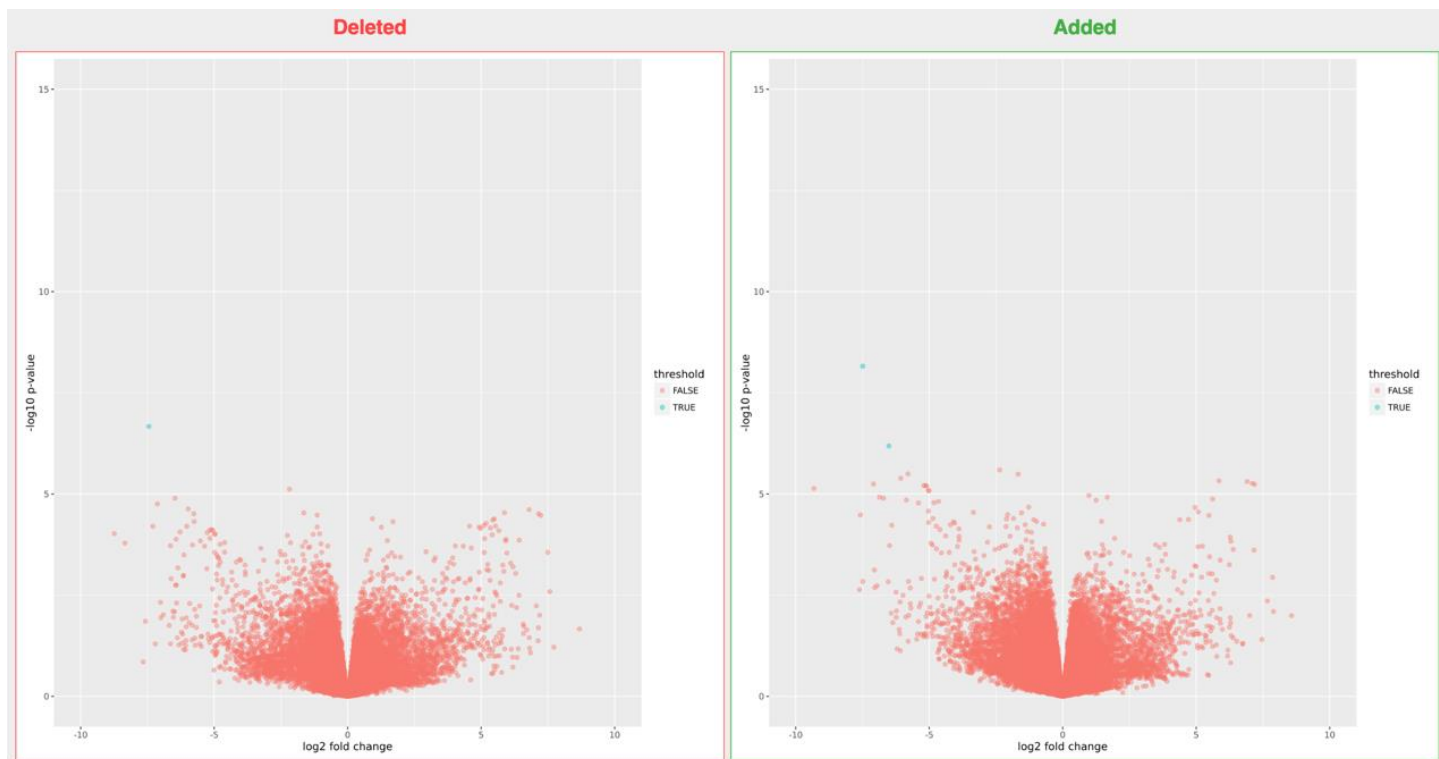
The effect of adding the HumanTw2 sequence to the constructed phylogenetic tree in two different continuous analysis runs.



Supplementary Figure 5

Principal component analysis plot of kallisto transcript quantification.

The effect of adding an additional organoid derived from pancreatic adenocarcinoma on principal components analysis using Kallisto's estimated counts.



Supplementary Figure 6

Differential expression analysis before and after adding an additional sample.

A volcano plot plotting the p-value vs. the log fold change. Adding an additional organoid derived from pancreatic adenocarcinoma leads to an additional gene being marked as significantly differentially expressed after Benjamini & Hochberg correction.